

Amendments to the Claims:

Please cancel claims 1-44, without prejudice to or disclaimer of the underlying subject matter, and please add the following claims 45-60:

1-44. (Cancelled)

45. (New) A method for determining a probability for one or more states for a selected nucleotide in a nucleic acid sequence, comprising:

a) determining an initial oligonucleotide probability for each of said states for an initial oligonucleotide in said nucleic acid sequence;

b) determining transition probabilities for each of said states for nucleotides within said nucleic acid sequence following said initial oligonucleotide;

c) using said initial oligonucleotide probability and said transition probabilities to determine a plurality of nucleic acid sequence probabilities, said plurality comprising a nucleic acid sequence probability corresponding to each of said states for said selected nucleotide; and,

d) applying a bias function to said plurality of nucleic acid sequence probabilities, to determine a probability for each of said states for said selected nucleotide, wherein said bias function does not have the same value in all of said states for said selected nucleotide.

46. (New) The method of claim 45, wherein said probability for each of said states for said selected nucleotide is determined using an inhomogeneous Markov model having eight states, wherein said eight states are: first reading frame positive strand (1+); second reading frame positive strand (2+); third reading frame positive strand (3+); first reading frame negative strand (1-); second reading frame negative strand (2-); third reading

frame negative strand (3-); noncoding positive strand (N+); and, noncoding negative strand (N-).

47. (New) The method of claim 46, wherein said probability for each of said eight states for said selected nucleotide is determined using the equation

$$P(f|S) = \frac{\phi(f) \cdot P_f \cdot P_f(S)}{\sum_{i \in \{1+, 2+, 3+, N+, 1-2-, 3-, N-\}} \phi(f) \cdot P_i \cdot P_i(S)}$$

48. (New) The method of claim 45, wherein said selected nucleotide is the middle nucleotide in said nucleic acid sequence.

49. (New) The method of claim 45, wherein said nucleic acid sequence is part of a longer nucleic acid sequence.

50. (New) The method of claim 45, wherein said bias function has a value between 0.0 and 0.9, or greater than 1.1, in one or more of said states for said selected nucleotide.

51. (New) A method for determining a probability for one or more states for a selected nucleotide in a nucleic acid sequence, comprising:

a) determining an initial oligonucleotide probability for each of said states for an initial oligonucleotide in said nucleic acid sequence;

b) determining transition probabilities for each of said states for nucleotides within said nucleic acid sequence following said initial oligonucleotide;

c) using said initial oligonucleotide probability and said transition probabilities to determine a plurality of nucleic acid sequence probabilities, said plurality comprising a

nucleic acid sequence probability corresponding to each of said states for said selected nucleotide; and,

d) determining a probability for each of said states for said selected nucleotide, wherein said determining a probability for each of said states accepts a bias function, and wherein said bias function does not have the same value in all of said states for said selected nucleotide.

52. (New) A method for determining a probability for each of one or more states for more than one selected nucleotide in a nucleic acid sequence comprising:

a) determining an initial oligonucleotide probability for each of said states for an initial oligonucleotide in a window of a first selected nucleotide;

b) determining transition probabilities for each of said states for nucleotides within said window following said initial oligonucleotide;

c) using said initial oligonucleotide probability and said transition probabilities to determine a plurality of window probabilities, wherein said plurality comprises a window probability corresponding to each of said states for said selected nucleotide;

d) applying a bias function to said plurality of window probabilities, to determine a probability for each of said states for said selected nucleotide, wherein said bias function does not have the same value in all of said states for said selected nucleotide; and,

e) repeating steps a) through d) for each remaining selected nucleotide in said nucleic acid sequence.

53. (New) The method of claim 52, wherein said more than one selected nucleotide are contiguous, and step e) is performed sequentially from said first selected nucleotide to a last selected nucleotide.

54. (New) The method of claim 53, wherein said probability for each of said states for said more than one selected nucleotide is determined using an inhomogeneous Markov model having eight states, wherein said eight states are: first reading frame positive strand (1+); second reading frame positive strand (2+); third reading frame positive strand (3+); first reading frame negative strand (1-); second reading frame negative strand (2-); third reading frame negative strand (3-); noncoding positive strand (N+); and, noncoding negative strand (N-).

55. (New) The method of claim 54, wherein said probability for each of said states for said more than one selected nucleotide is determined using the equation

$$P(f|S) = \frac{\phi(f) \cdot P_f \cdot P_f(S)}{\sum_{i \in \{1+, 2+, 3+, N+, 1-, 2-, 3-, N-\}} \phi(f) \cdot P_i \cdot P_i(S)}$$

56. (New) The method of claim 52, wherein said nucleic acid sequence is part of a longer nucleic acid sequence.

57. (New) The method of claim 52, wherein each selected nucleotide in said more than one selected nucleotide is the middle nucleotide in its own window.

58. (New) The method of claim 52, further comprising:

f) extending said nucleic acid sequence if said window extends beyond either end of said nucleic acid sequence, wherein said extending is accomplished by copying nucleotides from an end of said nucleic acid sequence at which said window is located to produce a copied nucleotide sequence, and adding said copied nucleotide sequence to said end.

59. (New) The method of claim 52, wherein said window has a length of about 75 to about 125 nucleotides.

60. (New) The method of claim 52, wherein said bias function has a value between 0.0 and 0.9, or greater than 1.1, in one or more of said states for said selected nucleotide.